

Sbjct: 898 ctggtactgccagatccagtagccggcccttctttccctgaccgccactctgggctggc 957

Query: 758 cggcttcaccctgctcctcagtcctcctggcctttgccatgtaccgcccgtagtgccctcg 817  
|||||

Sbjct: 958 cggcttcaccctgctcctcagtcctcctggcctttgccatgtaccgcccgtagtgccctcg 1017

Query: 818 cgggcgcttggcagcgtcgccggccctcctcggaccttgctccccgcgcgcggcgaggagc 877  
|||||

Sbjct: 1018 cgggcgcttggcagcgtcgccggccctcctcggaccttgctccccgcgcgcggcgaggagc 1077

Query: 878 tgetgcctgccagggccgcctctccggcctgcctcttcccgctgccctggagcccagcc 937  
|||||

Sbjct: 1078 tgetgcctgccagggccgcctctccggcctgcctcttcccgctgccctggagcccagcc 1137

Query: 938 ctgcgcgcagaggactcccgaggactggcggaggccccgcctgcgaccgccgggggctcg 997  
|||||

Sbjct: 1138 ctgcgcgcagaggactcccgaggactggcggaggccccgcctgcgaccgccgggggctcg 1197

Query: 998 gggccacctcccggggctgctgmcc-tcagcccgcaactgggagtgggctcctcggggtcg 1056  
|||||

Sbjct: 1198 gggccacctcccggggctgctgacctcagcccgcaactgggagtgggctcctcggggtcg 1257

Query: 1057 ggcattctgtgctgctgcctcgcccccgggcagagccggggccgcgcccgggggcccgctctt 1116  
|||||

Sbjct: 1258 ggcattctgtgctgctgcctcgcccccgggcagagccggggccgcgcccgggggcccgctctt 1317

Query: 1117 agtggtctgcggaggagccagccgcctccm-tccctgacagctccttgggctgagttgg 1175  
|||||

Sbjct: 1318 agtggtctgcggaggagccagccgcctccaatccctgacagctccttgggctgagttgg 1377

Query: 1176 ggacgccaggctcgggtgggaggctggtgm-ggggagcggggaggggcagaggagttccccg 1234  
|||||

Sbjct: 1378 ggacgccaggctcgggtgggaggctggtgaaggggagcggggaggggcagaggagttccccg 1437

Query: 1235 gm-cccgtgcagattw--gtm-ctgtgm-glitttaaaaaaaaaaaaaaaaaaaaaa 1281  
| |||||

Sbjct: 1438 gaaccctgcagattaaagtaactgtgaagttttcaaaaaaaaaaaaaaaaaaaaaa 1489

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281  
|||||


Sbjct: 1477 aaaaaaaaaaaaaaaaaaaaaa 1494

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281  
|||||||  
Sbjct: 1476 aaaaaaaaaaaaaaaaaaaaaa 1493

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281  
|||||||  
Sbjct: 1475 aaaaaaaaaaaaaaaaaaaaaa 1492

>gi|31543199|ref|NM\_031434.2|  Homo sapiens chromosome 7 open reading frame 2  
Length = 1494

Score = 2042 bits (1019), Expect = 0.0  
Identities = 1203/1252 (96%), Gaps = 28/1252 (2%)  
Strand = Plus / Plus

Query: 58 gctcggtagcgcgggcgggcm-ggcaggcgccatgaccctgattgm-ggggtgggtgatga 115  
|||||||  
Sbjct: 238 gctcggtagcgcgggcgggcaaggcaggcgccatgaccctgattgaaggggtgggtgatga 297

Query: 116 ggtgaccgtccttttctcggtgcttgccctgccttctggtgctggcccttgccctgggtctc 175  
|||||||  
Sbjct: 298 ggtgaccgtccttttctcggtgcttgccctgccttctggtgctggcccttgccctgggtctc 357

Query: 176 m-cgcacaccgctgagggcggggacccactgccccagccgtcagggaccccm-cgccatc 233  
|||||||  
Sbjct: 358 aacgcacaccgctgagggcggggacccactgccccagccgtcagggaccccaacgccatc 417

Query: 234 ccagcccagcgcgagccatggcagctaccgacagcatgagaggggaggccccaggggcaga 293  
|||||||  
Sbjct: 418 ccagcccagcgcgagccatggcagctaccgacagcatgagaggggaggccccaggggcaga 477

Query: 294 gacccccagcctgagacacagaggctcm-gctgcacagccagagcccagcacggggttcac 352  
|||||||  
Sbjct: 478 gacccccagcctgagacacagaggctcaagctgcacagccagagcccagcacggggttcac 537

Query: 353 agcm-caccgcccagccccggactccccgcaggagccccctcgtgctacggctgw--ttcct 409  
|||  
Sbjct: 538 agcaacaccgcccagccccggactccccgcaggagccccctcgtgctacggctgaaattcct 597

Query: 410 cm-tgattcagagcagggtggccagggccttgccccacgacaccattggctcettg----g 464  
| | |||||  
Sbjct: 598 caatgatcagagcagggtggccagggccttgccccacgacaccattggctcettgaaaag 657

Query: 465 gaccagtttcccggccgggm-cagcagggtgcgactcatctaccm-gggcagctgctagg 522  
|||||  
Sbjct: 658 gaccagtttcccggccgggaacagcagggtgcgactcatctaccaagggcagctgctagg 717

Query: 523 cgacgacaccagaccctgggcagccttcacctccctcccm-ctgcgttctccactgcc 581  
|||||  
Sbjct: 718 cgacgacaccagaccctgggcagccttcacctccctcccaactgcgttctccactgcc 777

Query: 582 cgtgtccacgagagtcggtcccccw--tccccctgcccgcgggggtccgagcccggccc 639  
|||||  
Sbjct: 778 cgtgtccacgagagtcggtcccccaaataccccctgcccgcgggggtccgagcccggccc 837

Query: 640 ctccgggctggw--tcggcagcctgctgctgcccctgctgctcctgctgttctgctget 697  
|||||  
Sbjct: 838 ctccgggctggaaatcggcagcctgctgctgcccctgctgctcctgctgttctgctget 897

Query: 698 ctggtactgccagatccagtaaccggcccttctttccctgaccgccactctgggcctggc 757  
|||||  
Sbjct: 898 ctggtactgccagatccagtaaccggcccttctttccctgaccgccactctgggcctggc 957

Query: 758 cggcttcaccctgctcctcagttctctggcctttgccaatgtaccgcccgtagtgccctcg 817  
|||||  
Sbjct: 958 cggcttcaccctgctcctcagttctctggcctttgccaatgtaccgcccgtagtgccctcg 1017

Query: 818 cgggcgcttggcagcgctgcgcggccctccggaccttgctccccgcgcgcggcgagg 877  
|||||  
Sbjct: 1018 cgggcgcttggcagcgctgcgcggccctccggaccttgctccccgcgcgcggcgagg 1077

Query: 878 tgctgcctgccagggccgcctctccggcctgctcttcccgctgccctggagcccagcc 937  
|||||  
Sbjct: 1078 tgctgcctgccagggccgcctctccggcctgctcttcccgctgccctggagcccagcc 1137

Query: 938 ctgcgcgcagaggactcccgggactggcggaggccccgccctgcgacgcgcggggctcg 997  
|||||  
Sbjct: 1138 ctgcgcgcagaggactcccgggactggcggaggccccgccctgcgacgcgcggggctcg 1197

Query: 998 gggccacctcccggggctgctgmcc--tcagcccgcaactgggagtgggctcctcggggtcg 1056  
|||||  
Sbjct: 1198 gggccacctcccggggctgctgacctcagcccgcaactgggagtgggctcctcggggtcg 1257

Query: 1057 ggcatctgctgtcgctgctcctcgccccgggcagagccggggccgccccgggggcccgtctt 1116  
|||||  
Sbjct: 1258 ggcatctgctgtcgctgctcctcgccccgggcagagccggggccgccccgggggcccgtctt 1317

Query: 1117 agtgttctgcccggaggaccagccgcctccm-tccctgacagctccttgggctgagttgg 1175  
 |||  
 Sbjct: 1318 agtgttctgcccggaggaccagccgcctccaatccctgacagctccttgggctgagttgg 1377

Query: 1176 ggacgccaggtcgggtgggaggtggtgm-ggggagcggggaggggcagaggagttccccg 1234  
 |||  
 Sbjct: 1378 ggacgccaggtcgggtgggaggtggtgaaggggagcggggaggggcagaggagttccccg 1437

Query: 1235 gm-cccgtgcagattw---gtm-ctgtgm-gttttaaaaaaaaaaaaaaaaaaaaa 1281  
 | |||  
 Sbjct: 1438 gaaccgtgcagattaaagtaactgtgaagttttcaaaaaaaaaaaaaaaaaaaaa 1489

Score = 36.6 bits (18), Expect = 125  
 Identities = 18/18 (100%)  
 Strand = Plus / Plus


Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281  
 |||  
 Sbjct: 1477 aaaaaaaaaaaaaaaaaaaaaa 1494

Score = 36.6 bits (18), Expect = 125  
 Identities = 18/18 (100%)  
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281  
 |||  
 Sbjct: 1476 aaaaaaaaaaaaaaaaaaaaaa 1493

Score = 36.6 bits (18), Expect = 125  
 Identities = 18/18 (100%)  
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281  
 |||  
 Sbjct: 1475 aaaaaaaaaaaaaaaaaaaaaa 1492

>gi|16756334|gb|AC010973.6|  Homo sapiens BAC clone RP11-148K1 from 7, complete s  
 Length = 222605

Score = 1395 bits (696), Expect = 0.0  
 Identities = 775/796 (97%), Gaps = 11/796 (1%)  
 Strand = Plus / Plus

Query: 464 ggacccagtttcccgccggg-mcagcaggtgcgactcatctacc-mgggcagctgctag 521  
 |||  
 Sbjct: 123794 ggacccagtttcccgccgggaacagcaggtgcgactcatctaccaagggcagctgctag 123853

Query: 522 ggcagcagaccccagaccctgggcagccttcacctccctccc-mctgcgttctccactgcc 580  
|||||  
Sbjct: 123854 ggcagcagaccccagaccctgggcagccttcacctccctcccaactgcgttctccactgcc 123913

Query: 581 acgtgtccacgagagtcgggtccccc--wtcccccctgccgcgcgggggtccgagcccggcc 638  
|||||  
Sbjct: 123914 acgtgtccacgagagtcgggtccccc aaatcccccctgccgcgcgggggtccgagcccggcc 123973

Query: 639 cctccgggctgg--wtccggcagcctgctgctgccctgctgctcctgctgttgctgctgc 696  
|||||  
Sbjct: 123974 cctccgggctggaaatccggcagcctgctgctgccctgctgctcctgctgttgctgctgc 124033

Query: 697 tctgggtactgccagatccagtagccggcccttctttccctgaccgccactctgggcctgg 756  
|||||  
Sbjct: 124034 tctgggtactgccagatccagtagccggcccttctttccctgaccgccactctgggcctgg 124093

Query: 757 ccggttcaccctgctcctcagtcctcctggcctttgccatgtaccgcccgtagtgccctcc 816  
|||||  
Sbjct: 124094 ccggttcaccctgctcctcagtcctcctggcctttgccatgtaccgcccgtagtgccctcc 124153

Query: 817 gcgggcgcttggcagcgtgcgcggccctccggaccttgctccccgcgcgcggggggag 876  
|||||  
Sbjct: 124154 gcgggcgcttggcagcgtgcgcggccctccggaccttgctccccgcgcgcggggggag 124213

Query: 877 ctgctgcctgccagggccgcctctccggcctgcctcttcccgcctggagcccagc 936  
|||||  
Sbjct: 124214 ctgctgcctgccagggccgcctctccggcctgcctcttcccgcgcctggagcccagc 124273

Query: 937 cctgcgcgcagaggactcccgggactggcgaggccccgcgcctgcgaccgcgggggctc 996  
|||||  
Sbjct: 124274 cctgcgcgcagaggactcccgggactggcgaggccccgcgcctgcgaccgcgggggctc 124333

Query: 997 ggggccacctcccggggctgctg-mcctcagcccgcaactgggagtgggctcctcgggggc 1055  
|||||  
Sbjct: 124334 ggggccacctcccggggctgctgacctcagcccgcaactgggagtgggctcctcgggggc 124393

Query: 1056 gggcatctgctgtcgtgcctcgccccgggcagagccggggccgccccggggggcccgctc 1115  
|||||  
Sbjct: 124394 gggcatctgctgtcgtgcctcgccccgggcagagccggggccgccccggggggcccgctc 124453

Query: 1116 tagtggtctgcccggaggaccagccgcctcc-mtccctgacagctccttgggctgagttg 1174  
|||||  
Sbjct: 124454 tagtggtctgcccggaggaccagccgcctccaatccctgacagctccttgggctgagttg 124513

Query: 1175 gggacgccaggtcggtgggaggctggtg-mggggagcggggaggggcagaggagttcccc 1233  
|||||  
Sbjct: 124514 gggacgccaggtcggtgggaggctggtgaaggggagcggggaggggcagaggagttcccc 124573

Query: 1234 gg-mcccgtgcagatt 1248  
|| |||||  
Sbjct: 124574 ggaacccgtgcagatt 124589

Score = 665 bits (332), Expect = 0.0  
Identities = 398/415 (95%), Gaps = 9/415 (2%)  
Strand = Plus / Plus

Query: 58 gctcggtagcgcggcgggcm-ggcaggcgccatgaccctgattgm-ggggtgggtgatga 115  
|||||  
Sbjct: 123101 gctcggtagcgcggcgggcaaggcaggcgccatgaccctgattgaaggggtgggtgatga 123160

Query: 116 ggtgaccgtccttttctcgggtgcttgccctgccttctggtgctggcccttgccctgggtctc 175  
|||||  
Sbjct: 123161 ggtgaccgtccttttctcgggtgcttgccctgccttctggtgctggcccttgccctgggtctc 123220

Query: 176 m-cgcacaccgctgagggcggggacccactgccccagccgtcagggaccccm-cgccatc 233  
|||||  
Sbjct: 123221 aacgcacaccgctgagggcggggacccactgccccagccgtcagggaccccaacgccatc 123280

Query: 234 ccagcccagcgcagccatggcagctaccgacagcatgagaggggaggccccaggggcaga 293  
|||||  
Sbjct: 123281 ccagcccagcgcagccatggcagctaccgacagcatgagaggggaggccccaggggcaga 123340

Query: 294 gacccccagcctgagacacagaggtc-mgctgcacagccagagccagcacgggggttcac 352  
|||||  
Sbjct: 123341 gacccccagcctgagacacagaggtaagctgcacagccagagccagcacgggggttcac 123400

Query: 353 agc-mcaccgccagccccggactccccgcaggagccccctcgtgctacggctg--wttcct 409  
||| |||||  
Sbjct: 123401 agcaacacgccagccccggactccccgcaggagccccctcgtgctacggctgaaattcct 123460

Query: 410 c-mtgattcagagcaggtggccagggcctggccccacgacaccattggctccttg 463  
| |||||  
Sbjct: 123461 caatgattcagagcaggtggccagggcctggccccacgacaccattggctccttg 123515

Score = 80.7 bits (40), Expect = 7e-12  
Identities = 48/50 (96%), Gaps = 1/50 (2%)  
Strand = Plus / Plus

Query: 10 cccgcccggm-gtgcccagaggggcccgcgatggagctgggggagccgggcg 58  
|||||  
Sbjct: 122212 cccgcccgaagtgcccgaggggcccgcgatggagctgggggagccgggcg 122261

Score = 42.6 bits (21), Expect = 1.9  
Identities = 21/21 (100%)  
Strand = Plus / Plus

Query: 1261 ttttaaaaaaaaaaaaaaaaaaaaaa 1281  
|||||  
Sbjct: 115287 ttttaaaaaaaaaaaaaaaaaaaaaa 115307

Score = 38.6 bits (19), Expect = 31  
Identities = 22/23 (95%)  
Strand = Plus / Plus

Query: 1259 gtttttaaaaaaaaaaaaaaaaaaaaaa 1281  
|||||  
Sbjct: 115286 gtttttaaaaaaaaaaaaaaaaaaaaaa 115308

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281  
|||||  
Sbjct: 218391 aaaaaaaaaaaaaaaaaaaaaa 218374

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281  
|||||  
Sbjct: 218390 aaaaaaaaaaaaaaaaaaaaaa 218373

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281  
|||||  
Sbjct: 218389 aaaaaaaaaaaaaaaaaaaaaa 218372

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
 |||  
 Sbjct: 136554 aaaaaaaaaaaaaaaaaa 136537

Score = 36.6 bits (18), Expect = 125  
 Identities = 18/18 (100%)  
 Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
 |||  
 Sbjct: 136553 aaaaaaaaaaaaaaaaaa 136536

Score = 36.6 bits (18), Expect = 125  
 Identities = 18/18 (100%)  
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
 |||  
 Sbjct: 115297 aaaaaaaaaaaaaaaaaa 115314

Score = 36.6 bits (18), Expect = 125  
 Identities = 18/18 (100%)  
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
 |||  
 Sbjct: 115296 aaaaaaaaaaaaaaaaaa 115313

Score = 36.6 bits (18), Expect = 125  
 Identities = 18/18 (100%)  
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
 |||  
 Sbjct: 115295 aaaaaaaaaaaaaaaaaa 115312

Score = 36.6 bits (18), Expect = 125  
 Identities = 18/18 (100%)  
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
 |||  
 Sbjct: 115294 aaaaaaaaaaaaaaaaaa 115311

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 115293 aaaaaaaaaaaaaaaaaaaa 115310

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 115292 aaaaaaaaaaaaaaaaaaaa 115309

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 109993 aaaaaaaaaaaaaaaaaaaa 109976

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 109992 aaaaaaaaaaaaaaaaaaaa 109975

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 109991 aaaaaaaaaaaaaaaaaaaa 109974

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 109990 aaaaaaaaaaaaaaaaaa 109973

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 109989 aaaaaaaaaaaaaaaaaa 109972

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 109988 aaaaaaaaaaaaaaaaaa 109971

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 109987 aaaaaaaaaaaaaaaaaa 109970

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 109986 aaaaaaaaaaaaaaaaaa 109969

Score = 36.6 bits (18), Expect = 125  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281  
|  
Sbjct: 109985 aaaaaaaaaaaaaaaaaa 109968

**BLASTN 2.2.8 [Jan-05-2004]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1079554228-18277-13018448633.BLASTQ3

**Query=**

(1281 letters)

**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

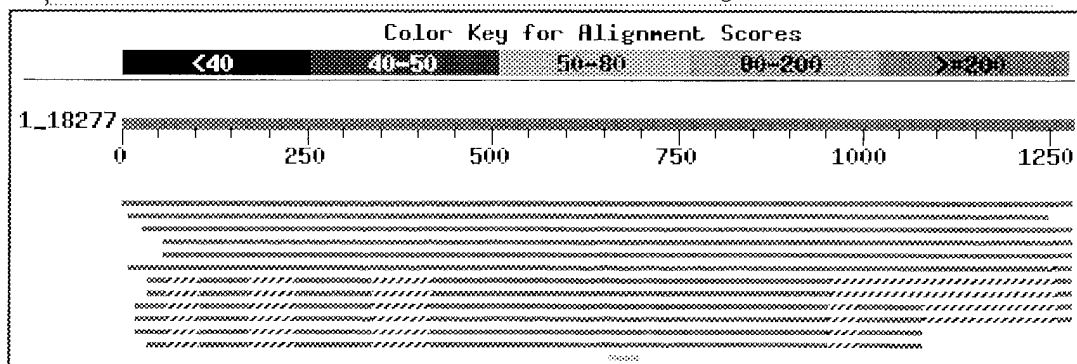
2,102,977 sequences; 10,130,642,339 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

### Distribution of 3783 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Query	Subject	Description	Score	E	Value
gi 37182084 gb AY358481.1	Homo sapiens clone DNA73744 TLIE...	2146	0.0		
gi 12654232 gb BC000936.1	Homo sapiens chromosome 7 open r...	2112	0.0		
gi 21303410 gb AY037155.1	Homo sapiens hypothetical membra...	2102	0.0		
gi 21620057 gb BC033182.1	Homo sapiens chromosome 7 open r...	2042	0.0		
gi 31543199 ref NM_031434.2	Homo sapiens chromosome 7 open...	2042	0.0		

<a href="#">gi 16756334 gb AC010973.6 </a>	Homo sapiens BAC clone RP11-148K...	<a href="#">1395</a>	0.0	
<a href="#">gi 37589845 gb BC059162.1 </a>	Rattus norvegicus Unknown (prote...	<a href="#">509</a>	e-141	
<a href="#">gi 38454297 ref NM_198781.1 </a>	Rattus norvegicus Unknown (pro...	<a href="#">509</a>	e-141	
<a href="#">gi 18043423 gb BC019547.1 </a>	Mus musculus RIKEN cDNA 20100040...	<a href="#">463</a>	e-127	
<a href="#">gi 12842087 dbj AK008109.1 </a>	Mus musculus adult male small i...	<a href="#">463</a>	e-127	
<a href="#">gi 7259235 dbj AB030183.1 </a>	Mus musculus mRNA, complete cds,...	<a href="#">463</a>	e-127	
<a href="#">gi 11967944 ref NM_022418.1 </a>	Mus musculus RIKEN cDNA 201000...	<a href="#">463</a>	e-127	
<a href="#">gi 2961613 gb AF051726.1 MMCATS1</a>	Mus musculus cathepsin S (...)	<a href="#">63</a>	2e-06	
<a href="#">gi 18873502 emb AL603702.14 </a>	Mouse DNA sequence from clone ...	<a href="#">63</a>	2e-06	
<a href="#">gi 21953265 emb AL591913.14 </a>	Mouse DNA sequence from clone ...	<a href="#">63</a>	2e-06	
<a href="#">gi 25013379 gb AC092203.16 </a>	Mus musculus chromosome 3 clone...	<a href="#">61</a>	7e-06	
<a href="#">gi 20068539 emb AL606742.11 </a>	Mouse DNA sequence from clone ...	<a href="#">61</a>	7e-06	
<a href="#">gi 22832231 gb AE003496.3 </a>	Drosophila melanogaster chromoso...	<a href="#">59</a>	3e-05	
<a href="#">gi 23172508 gb AE003766.2 </a>	Drosophila melanogaster chromoso...	<a href="#">59</a>	3e-05	
<a href="#">gi 15451484 gb AC022346.3 </a>	Drosophila melanogaster, chromos...	<a href="#">59</a>	3e-05	
<a href="#">gi 14028963 gb AC022343.2 AC022343</a>	Drosophila melanogaster,...	<a href="#">59</a>	3e-05	
<a href="#">gi 13676919 gb AC007827.5 AC007827</a>	Drosophila melanogaster,...	<a href="#">59</a>	3e-05	
<a href="#">gi 25455625 gb BC040122.1 </a>	Homo sapiens paired immunogloblin...	<a href="#">57</a>	1e-04	
<a href="#">gi 29791641 gb BC050547.1 </a>	Homo sapiens paired immunogloblin...	<a href="#">57</a>	1e-04	
<a href="#">gi 37361058 gb AC107662.9 </a>	Mus musculus chromosome 9, clone...	<a href="#">57</a>	1e-04	
<a href="#">gi 16551810 dbj AK056412.1 </a>	Homo sapiens cDNA FLJ31850 fis,...	<a href="#">57</a>	1e-04	
<a href="#">gi 20800363 gb AC025627.13 </a>	Homo sapiens chromosome 17, clo...	<a href="#">57</a>	1e-04	
<a href="#">gi 28201706 gb AC004448.3 </a>	Homo sapiens chromosome 17, clon...	<a href="#">57</a>	1e-04	
<a href="#">gi 5817856 gb AF161081.1 AF161081</a>	Homo sapiens activating r...	<a href="#">57</a>	1e-04	
<a href="#">gi 4508112 gb AC005071.2 AC005071</a>	Homo sapiens clone RG161A...	<a href="#">57</a>	1e-04	
<a href="#">gi 10441892 gb AF217981.1 AF217981</a>	Homo sapiens clone PP155...	<a href="#">57</a>	1e-04	
<a href="#">gi 6706622 emb AJ279565.1 HSA279565</a>	Homo sapiens genomic DN...	<a href="#">57</a>	1e-04	
<a href="#">gi 21739966 emb AL834336.1 HSM805391</a>	Homo sapiens mRNA; cDN...	<a href="#">57</a>	1e-04	
<a href="#">gi 21739928 emb AL834317.1 HSM805361</a>	Homo sapiens mRNA; cDN...	<a href="#">57</a>	1e-04	
<a href="#">gi 11932154 emb AJ400846.1 HSA400846</a>	Homo sapiens mRNA for ...	<a href="#">57</a>	1e-04	
<a href="#">gi 11932151 emb AJ400845.1 HSA400845</a>	Homo sapiens mRNA for ...	<a href="#">57</a>	1e-04	
<a href="#">gi 206982 gb M32515.1 RATSIMPB</a>	Rat simple sequence DNA, clo...	<a href="#">57</a>	1e-04	
<a href="#">gi 206979 gb M36626.1 RATSIMPA1</a>	Rat simple sequence DNA, cl...	<a href="#">57</a>	1e-04	
<a href="#">gi 30179910 ref NM_178238.1 </a>	Homo sapiens paired immunoglob...	<a href="#">57</a>	1e-04	
<a href="#">gi 30179914 ref NM_013440.3 </a>	Homo sapiens paired immunoglob...	<a href="#">57</a>	1e-04	
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<a href="#">gi 38564373 gb AC113203.10 </a>	Mus musculus chromosome 5, clon...	<a href="#">55</a>	5e-04	
<a href="#">gi 33147431 gb AC127256.4 </a>	Mus musculus BAC clone RP24-296G...	<a href="#">55</a>	5e-04	
<a href="#">gi 18043222 gb BC020026.1 </a>	Mus musculus cell division cycle...	<a href="#">55</a>	5e-04	
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<a href="#">gi 22138609 gb AC121903.2 </a>	Mus musculus BAC clone RP24-174G...	<a href="#">55</a>	5e-04	
<a href="#">gi 37951419 gb AC110240.8 </a>	Mus musculus chromosome 3, clone...	<a href="#">55</a>	5e-04	
<a href="#">gi 32421368 ref XM_331127.1 </a>	Neurospora crassa strain OR74A	<a href="#">55</a>	5e-04	
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<a href="#">gi 41351569 gb AC110219.11 </a>	Mus musculus chromosome 1, clon...	<a href="#">55</a>	5e-04	
<a href="#">gi 40557568 gb AY489267.1 </a>	Pinus sylvestris microsatellite ...	<a href="#">55</a>	5e-04	

<a href="#">gi 21614629 emb AL672218.9 </a>	Mouse DNA sequence from clone R...	55	5e-04	
<a href="#">gi 38050 emb X68361.1 MFAP0A4A</a>	M.fascicularis gene for apol...	55	5e-04	
<a href="#">gi 307289 gb L10375.1 HUMMRNAD</a>	Human (clone CTG-B10) mRNA s...	55	5e-04	
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<a href="#">gi 33439371 gb AY333202.1 </a>	Anopheles merus clone r2a micros...	53	0.002	
<a href="#">gi 33439365 gb AY333196.1 </a>	Anopheles gambiae clone b2bc mic...	53	0.002	
<a href="#">gi 33439364 gb AY333195.1 </a>	Anopheles gambiae clone b2a micr...	53	0.002	
<a href="#">gi 33439363 gb AY333194.1 </a>	Anopheles gambiae clone b1bc mic...	53	0.002	
<a href="#">gi 33439362 gb AY333193.1 </a>	Anopheles gambiae clone b1a micr...	53	0.002	
<a href="#">gi 33439361 gb AY333192.1 </a>	Anopheles gambiae clone s2ab mic...	53	0.002	
<a href="#">gi 33439360 gb AY333191.1 </a>	Anopheles gambiae clone s1ab mic...	53	0.002	
<a href="#">gi 14318643 gb BC009120.1 </a>	Mus musculus hypothetical protei...	53	0.002	
<a href="#">gi 23124364 gb AC093043.6 </a>	Mus Musculus Strain C57BL6/J Chr...	53	0.002	
<a href="#">gi 29423846 gb AC137055.12 </a>	Homo sapiens 12 BAC RP11-686G8 ...	53	0.002	
<a href="#">gi 29336195 gb AC040162.5 </a>	Homo sapiens chromosome 16 clone...	53	0.002	
<a href="#">gi 21166215 gb AC112516.2 </a>	Homo sapiens chromosome 3 clone ...	53	0.002	
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<a href="#">gi 23170582 gb AE003672.3 </a>	Drosophila melanogaster chromoso...	53	0.002	
<a href="#">gi 23093570 gb AE003540.3 </a>	Drosophila melanogaster chromoso...	53	0.002	
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<a href="#">gi 41529763 emb BX000463.18 </a>	Zebrafish DNA sequence from cl...	53	0.002	
<a href="#">gi 19880514 gb AF367096.1 </a>	Pinus taeda microsatellite RPTes...	53	0.002	
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<a href="#">gi 19880512 gb AF367094.1 </a>	Pinus taeda microsatellite RPTes...	53	0.002	
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<a href="#">gi 17571384 ref NG_000060.1 </a>	Drosophila melanogaster (sas)...	53	0.002	
<a href="#">gi 27151411 gb AC079245.35 </a>	Mus musculus chromosome 9 clone...	53	0.002	
<a href="#">gi 17028068 gb L47972.1 PIGTBBP</a>	Sus scrofa TATA box-binding...	53	0.002	
<a href="#">gi 15529033 gb AY044869.1 </a>	Homo sapiens p400 SWI2/SNF2-rela...	53	0.002	
<a href="#">gi 15451514 gb AC009462.6 </a>	Drosophila melanogaster, chromos...	53	0.002	
<a href="#">gi 15412432 gb AC091223.2 </a>	Drosophila melanogaster 3L BAC R...	53	0.002	
<a href="#">gi 15292268 gb AY051979.1 </a>	Drosophila melanogaster LD44801 ...	53	0.002	
<a href="#">gi 15278192 gb AF401656.1 AF401656</a>	Homo sapiens MAGI-1C bet...	53	0.002	
<a href="#">gi 15278185 gb AF401655.1 AF401655</a>	Homo sapiens MAGI-1A mRN...	53	0.002	
<a href="#">gi 15278181 gb AF401654.1 AF401654</a>	Homo sapiens MAGI-1B alp...	53	0.002	
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<a href="#">gi 30911038 emb AL929138.15 </a>	Mouse DNA sequence from clone ...	53	0.002	
<a href="#">gi 25058366 gb BC040029.1 </a>	Homo sapiens, clone IMAGE:575230...	53	0.002	
<a href="#">gi 22022302 dbj AB030728.1 </a>	Mus musculus gene for non-mitoc...	53	0.002	
<a href="#">gi 37958289 gb AY225906.1 </a>	Neurospora sp. FGSC 8847 microsa...	53	0.002	
<a href="#">gi 40354196 ref NM_020457.2 </a>	Homo sapiens THAP domain conta...	53	0.002	

## Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|37182084|gb|AY358481.1|](#) Homo sapiens clone DNA73744 TLIE763 (UNQ763) mRNA  
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Score = 2146 bits (1071), Expect = 0.0  
Identities = 1260/1310 (96%), Gaps = 29/1310 (2%)  
Strand = Plus / Plus

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Query: 60     tcggtagcgcggcgggc-mggcaggcgccatgacctgattg-mgggggtgggtgatgagg 117
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Sbjct: 61     tcggtagcgcggcgggcaaggcaggcgccatgacctgattgaaggggtgggtgatgagg 120

Query: 118    tgaccgtccttttctcggtgcttgccctgccttctggtgctggcccttgccctgggtctc-m 176
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Query: 355    c-mcaccgccagcccccggaactccccgcaggagccccctcgtgctacggctg--wtctctc- 410
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Sbjct: 361    caacaccgccagcccccggaactccccgcaggagccccctcgtgctacggctgaaattctcta 420

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Query: 525    acgacaccagaccctgggcagccttcacctccctccc-mctgcgttctccactgccacg 583
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Sbjct: 1261 acccgtgcagattaaagtaactgtgaagtttttaaaaaaaaaaaaaaaaaaaaaa 1310

 [gi112654232.gb|BC000936.11](http://gi112654232.gb|BC000936.11) Homo sapiens chromosome 7 open reading frame 2  
MGC:5442 IMAGE:3449979), complete cds  
Length = 1347

Score = 2112 bits (1054), Expect = 0.0  
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Strand = Plus / Plus

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 Strand = Plus / Plus

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Query: 668  gcccctgctgctcctgctggtgctgctgctctggtactgccagatccagtaccggccctt 727
          |||
Sbjct: 711  gcccctgctgctcctgctggtgctgctgctctggtactgccagatccagtaccggccctt 770

Query: 728  ctttccctgaccgccactctgggcctggccggcttcaccctgctcctcagtctcctggc 787
          |||
Sbjct: 771  ctttccctgaccgccactctgggcctggccggcttcaccctgctcctcagtctcctggc 830

Query: 788  ctttgccatgtaccgcccgtagtgccctccgcggcgcttggcagcgctgcgggcccctcc 847
          |||
Sbjct: 831  ctttgccatgtaccgcccgtagtgccctccgcggcgcttggcagcgctgcgggcccctcc 890

Query: 848  ggaccttgctccccgcgcgcggcgaggagctgctgctgcccaggcccgccctctccggcc 907
          |||
Sbjct: 891  ggaccttgctccccgcgcgcggcgaggagctgctgctgcccaggcccgccctctccggcc 950

Query: 908  tgccctcttcccgtgcccctggagcccagccctgcgcgcagaggactcccgggactggcg 967
          |||
Sbjct: 951  tgccctcttcccgtgcccctggagcccagccctgcgcgcagaggactcccgggactggcg 1010

Query: 968  gagggccccgccctgcgaccgcggggctcgggggccacctcccggggctgctgmcc-tcag 1026
          |||
Sbjct: 1011 gagggccccgccctgcgaccgcggggctcgggggccacctcccggggctgctgacctcag 1070

Query: 1027 cccgcactgggaglgggctcctcggggtcggggcactctgctgctgctgctcctcgggccccggg 1086
          |||
Sbjct: 1071 cccgcactgggagtgggctcctcggggtcggggcactctgctgctgctgctcctcgggccccggg 1130



Query: 1087 cagagccggggcgcgcgcgggggcccgtcttagtggttctgcccaggaggaccagccgcctcc 1146
          |||
Sbjct: 1131 cagagccggggcgcgcgcgggggcccgtcttagtggttctgcccaggaggaccagccgcctcc 1190

Query: 1147 m-tccctgacagctccttgggctgagttggggacgccaggctcggtgggaggctggtgm-g 1204
          |||
Sbjct: 1191 aatccctgacagctccttgggctgagttggggacgccaggctcggtgggaggctggtgaag 1250

Query: 1205 gggagcgggggaggggcagaggagttccccggm-cccgtgcagattw--gtm-ctgtgm-g 1259
          |||
Sbjct: 1251 gggagcgggggaggggcagaggagttccccggaaccctgacagattaaagtaactgtgaag 1310

Query: 1260 ttttaaaaaaaaaaaaaaaaaaaaaa 1281
          |||
Sbjct: 1311 ttttcaaaaaaaaaaaaaaaaaaaaaa 1332

```

 >gi|21620057|gb|BC033182.1|  Homo sapiens chromosome 7 open reading frame 21, MGC:45820 IMAGE:4586932), complete cds  
Length = 1494

Score = 2042 bits (1019), Expect = 0.0  
Identities = 1203/1252 (96%), Gaps = 28/1252 (2%)  
Strand = Plus / Plus

```
Query: 58      gctcggtagcgcggcggggcm-ggcaggcgccatgaccctgattgm-ggggtgggtgatga 115
               |||
Sbjct: 238      gctcggtagcgcggcgggcaaggcaggcgccatgaccctgattgaaggggtgggtgatga 297

Query: 116      ggtgaccgtccttttctcgggtgcttgccctgccttctggtgctggcccttgccctgggtctc 175
               |||
Sbjct: 298      ggtgaccgtccttttctcgggtgcttgccctgccttctggtgctggcccttgccctgggtctc 357

Query: 176      m-cgcacaccgctgagggcggggacccactgccccagccgtcagggaccccm-cgccatc 233
               |||
Sbjct: 358      aacgcacaccgctgagggcggggacccactgccccagccgtcagggaccccaacgccatc 417

Query: 234      ccagcccagcgcagccatggcagctaccgacagcatgagaggggagggccccaggggcaga 293
               |||
Sbjct: 418      ccagcccagcgcagccatggcagctaccgacagcatgagaggggagggccccaggggcaga 477

Query: 294      gacccccagcctgagacacagaggtcm-gctgcacagccagagcccagcacgggggttcac 352
               |||
Sbjct: 478      gacccccagcctgagacacagaggtcaagctgcacagccagagcccagcacgggggttcac 537

Query: 353      agcm-caccgccagccccggactccccgcaggagccccctcgtgctacggctgw--ttcct 409
               |||
Sbjct: 538      agcaacaccgccagccccggactccccgcaggagccccctcgtgctacggctgaaattcct 597

Query: 410      cm-tgattcagagcaggtggccagggcctggccccacgacaccattggctccttg---g 464
               |
Sbjct: 598      caatgattcagagcaggtggccagggcctggccccacgacaccattggctccttgaaaag 657

Query: 465      gacccagtttcccggccgggm-cagcaggtgcgactcatctaccm-gggcagctgctagg 522
               |||
Sbjct: 658      gacccagtttcccggccgggaacagcaggtgcgactcatctaccaagggcagctgctagg 717

Query: 523      cgacgacaccagaccctgggcagccttcacctccctcccm-ctgcgttctccactgcca 581
               |||
Sbjct: 718      cgacgacaccagaccctgggcagccttcacctccctcccaactgogttctccactgcca 777

Query: 582      cglgtccacgagagtggttccccw--tccccctgcccgccgggggtccgagcccggccc 639
               |||
Sbjct: 778      cgtgtccacgagagtcggttccccaaatccccctgcccgccgggggtccgagcccggccc 837

Query: 640      ctccgggctggw--tcggcagcctgctgctgccccctgctgctcctgctggttctgctgct 697
               |||
Sbjct: 838      ctccgggctggaaatcggcagcctgctgctgccccctgctgctcctgctggttctgctgct 897
```